

Title: US-10-005-647-1

RESULT 4

AF003927

LOCUS AF003927 3532 bp mRNA linear MAM 17-APR-2001  
DEFINITION Bos taurus D-glucuronyl C5 epimerase mRNA, complete cds.  
ACCESSION AF003927  
VERSION AF003927.2 GI:13654638

KEYWORDS

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 3532)  
AUTHORS Li, J., Hagner-McWhirter, A., Kjellen, L., Palgi, J., Jalkanen, M. and Lindahl, U.

TITLE Biosynthesis of heparin/heparan sulfate. cDNA cloning and expression of D-glucuronyl C5-epimerase from bovine lung

J. Biol. Chem. 272 (44), 28158-28163 (1997)

MEDLINE 98010666

PUBMED 9346972

REFERENCE 2 (bases 1 to 3532)

AUTHORS Li, J.-P. and Lindahl, U.

TITLE Direct Submission

JOURNAL Submitted (14-MAY-1997) Medical and Physiological Chemistry, Biomedical Center, Husargatan 3, Uppsala 751 23, Sweden

REFERENCE 3 (bases 1 to 3532)

AUTHORS Li, J.-P., Gong, F., Darwish, K.E.I., Jalkanen, M. and Lindahl, U.

TITLE Direct Submission

JOURNAL Submitted (26-FEB-2001) Medical Chemistry and Microbiology, Biomedical Center, Husargatan 3, Uppsala 751 23, Sweden

REMARK Sequence update by submitter

COMMENT On Apr 17, 2001 this sequence version replaced gi:2465198.

FEATURES

Location/Qualifiers

source 1. .3532

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="lung"

CDS 1. .1854

/function="heparin/heparan sulfate biosynthesis"

/codon\_start=1

/product="D-glucuronyl C5 epimerase"

/protein\_id="AAB72083.2"

/db\_xref="GI:13654639"

/translation="MRCLAARVNYKTLIIICALFTLVTVLLWNKSSDKAIQVPRHLS  
SGFRVDALEKKAASESNNYVNHMAKQSEEAFFPQEQKAPPVVGFFNNNGGGRVLGLK  
YEEIDCLINDEHTIKGRREGNEVFLPFTWVEKYFDVYGKVVQYDGYDRFEFSHSYSKV  
YAQRAPYHPDGVFMSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGL  
SHYSKNLTEKPPHIEVYETAEDRDKNKPNPDWTVPKGCFMASVADKSRFTNVKQFIAP  
ETSEGVSLQLGNTKDFIISFDLKFLTNGSVSVVLETTEKNQLFTVHYVSNTQLIAFKE  
RDIYYGIGPRTSWSTVTRDLVTDLRKGVGLSNTKAVKPTRIMPKKVRLIAKGKGFLD  
NITISTTAHMAAFFAASDWLVNRQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQQA  
ISTLVRAYLLTKDHIFLNSALRATAPYKFLSEQHGVKAVFMNKHWDWYEEYPTTPSSFV  
LNGFMYSLIGLYDLKETAGEKLGKEARSLYERGMSLKAMLPDYDTGSGTIYDLRHF  
LGIAPNLARWDYHTTHINQLQLLSTIDESPIFKEFVKRWKSYLKGSRAKHN"

ORIGIN

Query Match 85.1%; Score 1577.2; DB 4; Length 3532;  
Best Local Similarity 91.0%; Pred. No. 0;  
Matches 1688; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

Qy 1 ATGCGTTGTTTGGCAGCTCGGGTCAACTATAAGACTTTGATTATCATCTGTGCGCTATTC 60

|||||

Db 1 ATGCGTTGTTTGGCAGCTCGGGTCAACTATAAGACTCTGATTATCATCTGCGCACTCTTC 60

Qy	61	ACTTTGGTCACAGTACTTTTGTGGAATAAGTGTTCAGCGACAAAGCAATCCAGTTTCCT	120
Db	61	ACTTTGGTCACAGTACTTTTGTGGAATAAGTGTTCAGTGACAAAGCGATCCAGGTTCCA	120
Qy	121	CGGCACTTGAGTAGTGGATTGAGAGTGGATGGATTAGAAAAAAGATCAGCAGCATCTGAA	180
Db	121	CGGCACTTGAGTAGTGGCTTCAGAGTGGATGCCTTAGAAAAAAGCAGCAGCGTCTGAG	180
Qy	181	AGTAACCACTATGCCAACACATAGCCAAACAGCAGTCAGAAGAGGCATTTCTCAGGAA	240
Db	181	AGCAACAACCTATGTGAACCACATGGCCA---AGCAGTCTGAGGAGGCCTTCCCTCAGGAA	237
Qy	241	CAACAGAAGGCACCCCCTGTTGTTGGGGGCTTCAATAGCAACGGGGGAAGCAAGGTGTTA	300
Db	238	CAGCAGAAAAGCGCCCCTGTTGTTGGGGGCTTCAATAACAATGGGGGAGGCAGGGTGTTA	297
Qy	301	GGGCTCAAATATGAAGAGATTGACTGTCTCATAAACGATGAGCACACCATTAAGGGAGA	360
Db	298	GGGCTCAAATATGAAGAAATTGACTGCCTCATAAATGATGAACACACAATTAAAGGGAGA	357
Qy	361	CGAGAGGGGAATGAAGTTTTCTTCCATTCACTTGGGTAGAGAAATACTTTGATGTTTAT	420
Db	358	CGAGAGGGGAATGAAGTCTTTCTTCCATTACCTGGGTAGAGAAATATTTTGACGTTTAC	417
Qy	421	GGAAAAGTGGTCCAGTATGACGGCTATGATCGATTTGAATTCTCTCATAGCTATTCCAAA	480
Db	418	GGAAAGGTGGTTCAGTATGATGGCTATGATCGGTTTGAATTCTCTCATAGCTATTCCAAA	477
Qy	481	GTCTATGCACAGAGATCACCTTATCACCTGACGGTGTGTTTATGTCCTTTGAAGGCTAC	540
Db	478	GTCTATGCACAGAGAGCCCCTTATCACCTGATGGTGTGTTTATGTCCTTTGAAGGCTAC	537
Qy	541	AATGTGGAAGTCCGAGACAGAGTCAAATGTATAAGTGGAGTTGAAGGTGTGCCATTATCT	600
Db	538	AATGTGGAAGTCCGAGACAGAGTCAAGTGCATAAGTGGGGTTGAAGGTGTACCTTTATCT	597
Qy	601	ACCCAGTGGGGGCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGCTAAGT	660
Db	598	ACACAGTGGGGACCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGTAAAGT	657
Qy	661	CATTACAGCAAGAATCTAACCGAGAAACCCCCTCACATAGAAGTATATGAAACAGCAGAA	720
Db	658	CACTACAGCAAGAATCTAACTGAAAAACCCCCTCATATAGAGGTATATGAAACAGCAGAA	717
Qy	721	GACAGGGACAGAAACATCAGACCTAATGAATGGACTGTGCCCAAGGGGTGCTTCATGGCC	780
Db	718	GACAGGGACAAAAACAGCAAGCCCAATGACTGGACTGTGCCCAAGGGGTGCTTTATGGCT	777
Qy	781	AGTGTGGCAGACAAGTCTAGATCCACCAATGTTAAACAGTTTATTGCTCCAGAAACAGT	840
Db	778	AGTGTGGCTGATAAGTCAAGATTACCAATGTTAAACAGTTCATTGCTCCAGAAACAGT	837
Qy	841	GAAGGTGTGTCTTTGCAGCTGGGAAACACAAAAGACTTCATTATTTTCACTTGACCTCAAG	900
Db	838	GAAGGTGTATCCTTGCAACTGGGGAACACAAAAGATTATTATTTCATTTGACCTCAAG	897
Qy	901	CTTTTAACAAATGGGAGTGTGTCTGTGGTTCTGGAGACCACAGAAAAGAATCAGCTCTTC	960
Db	898	TTCTTAACAAATGGAAGCGTGTCTGTGGTTCTGGAGACGACAGAAAAGAATCAGCTCTTC	957
Qy	961	ACTGTGCATTATGTCTCAAACACCCAGCTGATTGCTTTCAGAGACAGGGACATATACTAC	1020
Db	958	ACTGTACATTATGTCTCAAATACCCAGCTAATTGCTTTTAAAGAAAGAGACATATACTAT	1017
Qy	1021	GGCATTGGGCCCAGAACTTCATGGAGTACAGTTACCAGAGACCTGGTCACTGACCTCAGG	1080
Db	1018	GGCATCGGGCCCAGAACATCATGGAGCACAGTTACCCGGGACCTGGTCACTGACCTCAGG	1077

Qy	1081	AAAGGAGTGGGCCTTTCTAACACAAAAGCTGTCAAGCCAACCAAAATCATGCCCAAAAAAG	1140
Db	1078	AAAGGAGTGGGTCTTTCCAACACAAAAGCTGTCAAGCCAACAAGAATAATGCCCAAGAAG	1137
Qy	1141	GTGGTTAGGTTGATTGCAAAAGGGAAGGGATTCTCGGACAACATTACCATCTCAACCACA	1200
Db	1138	GTGGTTAGGTTGATTGCGAAAGGGAAGGGCTTCCTTGACAACATTACCATCTCTACCACA	1197
Qy	1201	GCCCACATGGCTGCATTCTTTGCTGCAAGTGACTGGCTAGTGAGGAACCAGGATGAGAAA	1260
Db	1198	GCCCACATGGCTGCCTTCTTCGCTGCCAGTGACTGGCTGGTGAGGAACCAGGATGAGAAA	1257
Qy	1261	GGTGGCTGGCCAATTATGGTGACCCGGAAGTTAGGGGAAGGGTTTAAATCTTTAGAACCA	1320
Db	1258	GGCGGCTGGCCGATTATGGTGACCCGTAAGTTAGGGGAAGGCTTCAAGTCTTTAGAGCCA	1317
Qy	1321	GGATGGTACTCTGCCATGGCACAAGGGCAAGCCATCTCTACCTTAGTCAGGGCCTATCTT	1380
Db	1318	GGGTGGTACTCCGCCATGGCCAAGGGCAAGCCATTTCTACATTAGTCAGGGCCTATCTC	1377
Qy	1381	CTAACGAAAGACTATGTATTCTCAGTTCAGCTTTAAGGGCAACAGCCCCATACAAGTTT	1440
Db	1378	TTAACAAAAGACCATATATTCTCAATTCAGCTTTAAGGGCAACAGCCCCTTACAAGTTT	1437
Qy	1441	CCGTCAGAGCAGCATGGAGTTAAAGCCGTGTTTCATGAATAAACATGACTGGTATGAAGAA	1500
Db	1438	CTGTCAGAGCAGCATGGAGTCAAGGCTGTGTTTATGAATAAACATGACTGGTATGAAGAA	1497
Qy	1501	TATCCAACCACACCTAGCTCTTTTGTTTTAAATGGCTTTATGTATTCTTTAATTGGGCTG	1560
Db	1498	TATCCAACCTACACCTAGCTCTTTTGTTTTAAATGGCTTTATGTATTCTTTAATTGGGCTG	1557
Qy	1561	TATGACCTAAAAGAAACAGCAGGGGAGACACTTGGGAAAGAAGCAAGGTCCTTGTACGAG	1620
Db	1558	TATGACTTAAAAGAAACTGCAGGGGAAAAACTCGGGAAAGAAGCGAGGTCCTTGTATGAG	1617
Qy	1621	CGCGGCATGGAATCTCTTAAAGCCATGCTGCCCTTGATGATACTGGCTCCGGGACCATC	1680
Db	1618	CGTGGCATGGAATCCCTTAAAGCCATGCTCCCCTTGATGATACTGGCTCAGGAACCATC	1677
Qy	1681	TATGACCTCCGCCACTTCATGCTTGGCATTGCTCCCAACCTGGCCCGCTGGGACTATCAC	1740
Db	1678	TATGACCTCCGGCACTTCATGCTTGGCATTGCCCCAACCTGGCCCGCTGGGACTATCAC	1737
Qy	1741	ACCACCCACATTAACCAGCTGCAGCTGCTCAGCACCATCGATGAGTCCCCAATCTTCAA	1800
Db	1738	ACCACCCACATCAATCAACTGCAGCTGCTTAGCACCATTGATGAGTCCCCAATCTTCAA	1797
Qy	1801	GAATTTGTCAAGAGGTGGAAAAGCTACCTTAAAGGCAGTAGGGCAAAGCACAAC	1854
Db	1798	GAATTTGTCAAGAGGTGGAAGAGCTACCTTAAAGGCAGCCGGGCAAAGCACAAC	1851

Title: US-10-005-647-2

RESULT 6

AAW79263

ID AAW79263 standard; protein; 444 AA.

XX

AC AAW79263;

XX

DT 15-FEB-1999 (first entry)

XX

DE Bovine glucuronyl C5-epimerase.

XX

KW Glucuronyl C5-epimerase; cattle; D-glucuronic acid; L-iduronic acid;

KW heparin; heparan sulphate.

XX

OS Bos taurus.

XX

FH Key Location/Qualifiers

FT Region 25. .45

FT /note= "potential transmembrane region"

FT Modified-site 51

FT /note= "N-glycosylated"

FT Modified-site 130

FT /note= "N-glycosylated"

FT Modified-site 220

FT /note= "N-glycosylated"

XX

PN WO9848006-A1.

XX

PD 29-OCT-1998.

XX

PF 17-APR-1998; 98WO-SE000703.

XX

PR 18-APR-1997; 97SE-00001454.

XX

PA (LIND/) LINDAHL U.

PA (LIJJ/) LI J.

XX

PI Lindahl U, Li J;

XX

DR WPI; 1998-583655/49.

DR N-PSDB; AAV62688.

XX

PT DNA sequence coding for mammalian glucuronyl C5-epimerase and functional

PT derivatives - capable of converting D-glucuronic acid to L-iduronic acid

PT in the synthesis of heparin and heparan sulphate.

XX

PS Disclosure; Page 18-19; 26pp; English.

XX

CC This is the amino acid sequence of bovine glucuronyl C5-epimerase. It was  
CC deduced from the sequence (see AAV62688) of a cDNA clone obtained from a  
CC bovine lung cDNA library. Glucuronyl C5-epimerase catalyses the  
CC conversion of D-glucuronic acid (GlcA) to L-iduronic acid (IdoA). The  
CC invention relates to isolated or recombinant DNA sequences for a  
CC mammalian (including human) glucuronyl C5-epimerase or its functional  
CC derivative. Recombinant expression vectors and transformed host cells are  
CC also claimed. The nucleic acid and vector can be used for the recombinant  
CC production of the enzyme. Glucuronyl C5-epimerase is useful for  
CC converting GlcA to IdoA in the biosynthesis of heparin and heparan  
CC sulphate

XX

SQ Sequence 444 AA;

Query Match 69.6%; Score 2271; DB 2; Length 444;

Best Local Similarity 96.8%; Pred. No. 1.3e-203;

Matches 430; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy	175	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	234
Db	1	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	60
Qy	235	VYETAEDRDRNIRPNEWTVPKGCFCMASVADKSRSTNVKQFIAPETSEGVSLQLGNTKDFI	294
Db	61	VYETAEDRDKNSKPNDWTVPKGCFCMASVADKSRFTNVKQFIAPETSEGVSLQLGNTKDFI	120
Qy	295	ISFDLKLTLNGSVSVVLETTTEKNQLFTVHYVSNTQLIAFRDRDIYYGIGPRTSWSTVTRD	354
Db	121	ISFDLKFLTNGSVSVVLETTTEKNQLFTVHYVSNTQLIAFKERDIYYGIGPRTSWSTVTRD	180
Qy	355	LVTDLRKGVGLSNTKAVKPTKIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV	414
Db	181	LVTDLRKGVGLSNTKAVKPTRIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV	240
Qy	415	RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQQAISTLVRAYLLTKDYVFLSSALRA	474
Db	241	RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQQAISTLVRAYLLTKDHIFLNSALRA	300
Qy	475	TAPYKFPSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGETLGKE	534
Db	301	TAPYKFLSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGEKLGKE	360
Qy	535	ARSLYERGMESLKAMPLDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID	594
Db	361	ARSLYERGMESLKAMPLDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID	420
Qy	595	ESPIFKEFVKRWKSYLKGSRAKHN	618
Db	421	ESPIFKEFVKRWKSYLKGSRAKHN	444

RESULT 15

US-09-403-269-13

; Sequence 13, Application US/09403269

; GENERAL INFORMATION:

; APPLICANT: ULF, Lindahl

; APPLICANT: LI, Jin-Ping

; TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a

; TITLE OF INVENTION: Process for Its Production

; FILE REFERENCE: 003300-589

; CURRENT APPLICATION NUMBER: US/09/403,269

; CURRENT FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: SE 9701454-2

; PRIOR FILING DATE: 1997-04-18

; PRIOR APPLICATION NUMBER: PCT/SE98/00703

; PRIOR FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Human

US-09-403-269-13

Query Match 69.6%; Score 2271; DB 18; Length 444;  
 Best Local Similarity 96.8%; Pred. No. 3e-220;  
 Matches 430; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy	175	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	234
Db	1	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	60
Qy	235	VYETAEDRDRNIRPNEWTVPKGCFCMASVADKSRSTNVKQFIAPETSEGVSLQLGNTKDFI	294
Db	61	VYETAEDRDKNSKPNDWTVPKGCFCMASVADKSRFTNVKQFIAPETSEGVSLQLGNTKDFI	120

Qy 295 ISFDLKLTLNGSVSVVLETTEKNQLFTVHYVSNTQLIAFRDRDIYYGIGPRTSWSTVTRD 354  
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 Db 121 ISFDLKLTLNGSVSVVLETTEKNQLFTVHYVSNTQLIAFKERDIYYGIGPRTSWSTVTRD 180  
 Qy 355 LVTDLRKGVGLSNTKAVKPTKIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV 414  
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 Db 181 LVTDLRKGVGLSNTKAVKPTRIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV 240  
 Qy 415 RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQAISTLVRAYLLTKDYVFLSSALRA 474  
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 Db 241 RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQAISTLVRAYLLTKDHFILNSALRA 300  
 Qy 475 TAPYKFPSEQHGKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGETLGKE 534  
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 Db 301 TAPYKFLSEQHGKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGEKLGKE 360  
 Qy 535 ARSLYERGMESLKAMLPDYTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID 594  
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 Db 361 ARSLYERGMESLKAMLPDYTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID 420  
 Qy 595 ESPIFKEFVKRWKSYLKGSRAKHN 618  
 |||||  
 Db 421 ESPIFKEFVKRWKSYLKGSRAKHN 444

# RESULT 1

## GLCE\_MOUSE

ID GLCE\_MOUSE STANDARD; PRT; 618 AA.  
 AC Q9EPS3; Q99MM0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE D-glucuronyl C5-epimerase (EC 5.1.3.-) (Heparin/heparan  
 DE sulfate:glucuronic acid C5 epimerase).  
 GN GLCE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.  
 RC STRAIN=BALB/c; TISSUE=Liver, and Mast cells;  
 RX MEDLINE=21282921; PubMed=11274177;  
 RA Li J.-P., Gong F., El Darwish K., Jalkanen M., Lindahl U.;  
 RT "Characterization of the D-glucuronyl C5-epimerase involved in the  
 RT biosynthesis of heparin and heparan sulfate."  
 RL J. Biol. Chem. 276:20069-20077(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC TISSUE=Mast cells;  
 RX MEDLINE=21293046; PubMed=11279150;  
 RA Crawford B.E., Olson S.K., Esko J.D., Pinhal M.A.S.;  
 RT "Cloning, Golgi localization, and enzyme activity of the full-length  
 RT heparin/heparan sulfate-glucuronic acid C5-epimerase."  
 RL J. Biol. Chem. 276:21538-21543(2001).  
 CC -!- FUNCTION: Converts D-glucuronic acid residues adjacent to N-  
 CC sulfate sugar residues to L-iduronic acids.  
 CC -!- PATHWAY: Heparin and heparan sulfate biosynthesis.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi.  
 CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in lung  
 CC and lowest levels in spleen.  
 CC -!- SIMILARITY: Belongs to the D-glucuronyl C5-epimerase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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